

FIG. 1A

1 CTGCTTCCACAGCAAGACACGACTGGAGAGCCGAGCCGGAGCAGCTGGGAAACATG
 -----+-----+-----+-----+-----+-----+-----+
 GACGAAGGTGGTCGTTTCTGGTGCTGACCTCTCGGCTCGGCCCTCGTCGACCCCTTTGTAC
 M

60

61 AAGAGCGTCTTGCTGACCACGCTCCTCGTGCCCTGCACACCTGGTGGCCGCTGGAGC
 -----+-----+-----+-----+-----+-----+-----+
 TTCTGCGAGAACGACGACTGGTGGGAGGAGCAGGACGTGTGGACCACCGCGGACCTCG
K S V L L L T T L L V P A H L V A A W S

120

121 AATAATTATGCGGTGGACTGCCCTCAACACTGTGACAGCAGTGAGTGCAAAAGCAGCCCG
 -----+-----+-----+-----+-----+-----+-----+
 TTATTAATACGCCACCTGACGGGAGTGTGACACTGTGCTCACTCACGTTTTCGTGGGC
 N N Y A V D' C P Q H C D S S E C K S S P

180

181 CGCTGCAAGAGGACAGTGCTCGACGACTGTGGCTGCTGCCGAGTGTCCGCTGCAGGGCGG
 -----+-----+-----+-----+-----+-----+-----+
 GCGACGTTCTCCTGTCACGAGCTGCTGACACCGACGAGCGGCTCACACGCGACGTCCCCGCC
 R C K R T V L D D C C G C C R V C A A G R

240

725

FIG. 1D

781 CATCCATATGACTGAACACTTGTATGTGTTGTTAAATATTCGAATGCATGTAGATTGT
-----+-----+-----+-----+-----+-----+
840 GTAGGTATACTGACTTGTGAACATACACAAACAATTATTAAGCTTACGTACATCTAAACA

841 TAAATGCTGTGTATAGTAACACTGAAGAACTAAAAATGCAATTTAGGTAATCTTACATG
-----+-----+-----+-----+-----+-----+
900 ATTTACACACACATATCATTTGTGACTTCTTGATTTTACGTTAAATCCATTAGAATGTAC

901 GAGACAGGTCAACCAAGAGGGAGCTAGGCCAAAGCTGAAGACCCGACGTAGTCAAAATTAG
-----+-----+-----+-----+-----+-----+
960 CTCGTCCAGTTGGTTTCTCCCTCGATCCGTTTCGACTTCTGGCGTCACTCAGTTTAATC

961 TTCTTTGACTTTTGATGTACATTAAATGTTGGGATATGGAATGAAGACTTAAGAGCAGGAGA
-----+-----+-----+-----+-----+-----+
1020 AAGAACTGAAACTACATGTAAATTACAACCCCTATACCTTACTTCTGAATTCTCGTCCTCT

1021 AGATGGGGAGGGGTGGGAGTGGGAAATAAAATATTAGCCCTTCCTTGGTAGTAGCTT
-----+-----+-----+-----+-----+-----+
1080 TCTACCCCTCCCCCACCCTCACCCCTTTATTTTATAAATCGGGAAGGAACCATCCATCGAA

NTCTNAAGGAC
-----+
NAGANTTCCTG

FIG. 2

ce10_chick	1	...	MGSAGAR	P	ALAAALLC	LARLALGSPC	PAV	...	CQC	...	PAA	APQ	50
cyr6_mouse		...	MSSSTR	TLAVAVTLAH	LTRLAL	STC	PAA	...	CHC	...	PLE	APK	
ctgf_human		...	MTAASMGPI	RVAFVLLAL	CSRPAVGQNC	SGP	...	CRC	...	PDEPAPR			
fisp-12		...	MLASVAGPI	SLAL	VLLAL	CTRATGQDC	SAQ	...	CQC	...	AAEAAPH		
nov_chick		...	METGGGQGL	PVLLLLLLL	RPCEVSGREA	ACPRPCGGRC	...	PAEP	PR				
ibp_3human		...	MQRARPTLWA	AALTLLVLLR	GPPVARAGAS	SGGLGPVVRC	EPCVARALAR						
ccn-4	MK	SVLLLTLLV	PAHLVAAWSN	MYAVDCPQHC	DSSECKSSPR						

ce10_chick	51	CAPGVGLVP	...	DGCGCC	KVCAKQLNED	C	...	SRTQP	CDHTKGLECN	100
cyr6_mouse		CAPGVGLVR	...	DGCGCC	KVCAKQLNED	C	...	SKTQP	CDHTKGLECN	
ctgf_human		CPAGVSLVL	...	DGCGCC	RVCAKQLGEL	C	...	TERDP	CDPHKGLFCD	
ccn-4		

ce10_chick	401	RLVNDIHKFR	D	411
cyr6_mouse		SLFNDIHKFR	D	
ctgf_human		YYRKMYGDMA	.	
fisp-12		YYRKMYGDMA	.	
nov_chick		DPMSEAKI	.	
ibp3_human		
ccn-4		